REMARKS

Applicants hereby elect, without traverse, the subject matter of Group I (claims 1-3, 5-7, and 91) drawn to a recombinant expression construct to lower Gly m Bd 30K (soybean vacuolar protein P34). This election is made subject to Applicants' right to pursue the non-elected subject matter in a divisional or divisional applications pursuant to 35 USC §121.

Claims 4, 8-90 have been canceled without prejudice to or disclaimer of the subject matter recited therein as being drawn to a non-elected invention.

Claims 1-3, 5-7, and 91 are now pending, with claims 1 and 3 being independent claims.

Claim 7 has been amended and claim 91 added to correct the multiple dependent claim objection of claim 7 under 37 CFR 1.75(c). Thus, no new matter has been added.
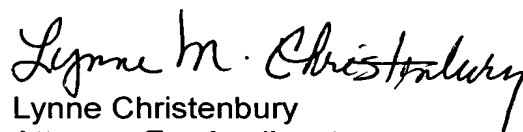
The specification has been amended at two locations to remove reference to the following URL: www.ncbi.nlm.nih.gov/BLAST/.

A petition for a two (2) month extension of time and version with markings to show changes made accompany this response.

Please charge the fee for a two (2) month extension of time and any other fees that may be associated with the filing of this response to Deposit Account No. 04-1928 (E. I. du Pont de Nemours and Company).

In view of the foregoing, allowance of the above-referenced application is respectfully requested.

Respectfully submitted,

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Dated: Dec. 20, 2002

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In showing the changes, deleted material is shown within brackets, and inserted material is shown underlined.

IN THE CLAIMS:

7. (once amended) Seeds of the plant of Claim 5[or 6].

91. (new) Seeds of the plant of Claim 6.

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IN THE SPECIFICATION:

Paragraph at page 9, lines 10-16:

A "substantial portion" of an amino acid or nucleotide sequence comprises enough of the amino acid sequence of a polypeptide or the nucleotide sequence of a gene to afford putative identification of that polypeptide or gene, either by manual evaluation of the sequence by one skilled in the art, or by computer-automated sequence comparison and identification using algorithms such as BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol. 215*:403-410) and Gapped Blast (Altschul, S. F., et al., (1997) Nucleic Acids Res. 25:3389-3402)[; see also www.ncbi.nlm.nih.gov/BLAST/)].

Paragraph at page 32, lines 19 through 35:

cDNA clones encoding soybean allergens were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol. 215*:403-410[; see also www.ncbi.nlm.nih.gov/BLAST/]) searches for similarity to sequences contained in the BLAST "nr" database (comprising all non-redundant GenBank CDS translations, sequences derived from the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The cDNA sequences obtained in Example 1 were analyzed for similarity to all publicly available DNA sequences contained in the "nr" database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the "nr" database using the BLASTX algorithm (Gish and

States (1993) *Nat. Genet. 3*:266-272) provided by the NCBI. For convenience, the P-value (probability) of observing a match of a cDNA sequence to a sequence contained in the searched databases merely by chance as calculated by BLAST are reported herein as "pLog" values, which represent the negative of the logarithm of the reported P-value. Accordingly, the greater the pLog value, the greater the likelihood that the cDNA sequence and the BLAST "hit" represent homologous proteins.